

# SEQUENCE LISTING

<110> Hepgenics Pty Ltd

<120> VIRAL VECTORS EXPRESSING FUSION OF VIRAL LARGE ENVELOPE  
PROTEIN AND PROTEIN OF INTEREST

<130> 19242

<140> 10/553,683

<141> 2005-10-17

<150> AU 2003901876

<151> 2003-04-17

<160> 13

<170> PatentIn version 3.2

<210> 1

<211> 25

<212> DNA

<213> duck

<400> 1

gggcaacatc cagcaaaatc aatgg

25

<210> 2

<211> 30

<212> DNA

<213> Homo sapiens

<400> 2

gctgcggaat ggctaaaagg gcccccgacc

30

<210> 3

<211> 34

<212> DNA

<213> Homo sapiens

<400> 3

ccaacactag atcacgaaac ccacgtcacc gggg

34

<210> 4

<211> 34

<212> DNA

<213> Homo sapiens

<400> 4

ggttgatgc tagtgctttg ggtgcagtgg cccc

34

<210> 5

<211> 3021

<212> DNA

<213> duck

<400> 5

catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggctaggaga

60

ttgctttggt ggcattacaa ctgtttactg tggggagaag ctcaagttac taactatatt

120

tctcgtttgc	gtacttggtt	gtcaactcct	gagaaatata	gaggtagaga	tgccccgacc	180
attgaagcaa	tcactagacc	aatccaggtg	gctcagggag	gcagaaaaac	aactacgggt	240
actagaaaac	ctcgtggact	cgaacctaga	agaagaaaag	ttaaaaccac	agttgtctat	300
gggagaagac	gttcaaagtc	ccgggaaagg	agagccccta	cacccaacg	tgcgggctcc	360
cctctccac	gtagttcgag	cagccaccat	agatctccct	cgctaggaa	ataaattacc	420
tgctaggcat	cacttaggta	aattgtcagg	actatatcaa	atgaagggt	gtacttttaa	480
cccagaatgg	aaagtaccag	atatttcgga	tactcatttt	aatttagatg	tagttaatga	540
gtgcccttcc	cgaaattgga	aatatttgac	tccagccaaa	ttctggccca	agagcatttc	600
ctactttcct	gtccaggtag	gggttaaacc	aaagtatcct	gacaatgtga	tgcaacatga	660
atcaatagta	ggtaaataatt	taaccaggct	ctatgaagca	ggaatccttt	ataagcggat	720
atctaaacat	ttggtcacat	ttaaaggcca	gccttataat	tggaacagc	aacaccttgt	780
caatcaacat	cacatttatg	atggggcaac	atccagcaaa	atcaatggac	gtcagacgga	840
tagaaggagg	agaaatactg	ttaaaccaac	ttgccggaag	gatgatccca	aaagggactt	900
tgacatggtc	aggcaagttt	ccaacactag	atcacgtgtt	agaccatgtg	caaacaatgg	960
aggagataaa	caccctccag	aatcagggag	cttggcctgc	tggggcgga	aggagagtag	1020
gattatcaaa	tccgactcct	caagagattc	ctcagcccca	gtggactccc	gaggaagacc	1080
aaaaagcacg	cgaagctttt	cgccgttatc	aagaagaaag	accaccgga	accaccacca	1140
ttcctccgtc	ttcccctcct	cagtgggaagc	tacaaccggg	ggacgatcca	ctcctgggaa	1200
atcagtctct	cctcgagact	catccgctat	accagtcaga	accagcgggtg	ccagtataa	1260
aaactcccc	cttgaagaag	aaaatgtctg	gtaccttcgg	gggaatacta	gctggcctaa	1320
tcggattact	ggtaagcttt	ttcttggtga	taaaaattct	agaaatactg	aggaggctag	1380
attggtggtg	gatttctctc	agttctccaa	agggaaaaat	gcaatgcgct	ttccaagata	1440
ctggagccca	aatctctcca	cattacgtag	gatcttgccc	gtggggatgc	ccaggatttc	1500
tttgaccta	tctcaggctt	tttatcatct	tcctcttaat	cctgctagta	gcagcaggct	1560
tgctgtatct	gacggacaac	gggtctacta	ttttaggaaa	gctccaatgg	gcgtcgggtct	1620
cagccctttt	ctcctccatc	tcttcactac	tgccctcgga	tccgaaatct	ctcgtcgctt	1680
taacgttttg	actttcactt	atatggatga	cttcctcctc	tgccacccaa	acgctcgtca	1740
ccttaacgca	attagccacg	ctgtctgctc	ttttttacaa	gagttaggaa	taagaataaa	1800
ctttgacaaa	accacgcctt	ctccggtgaa	tgaaataaga	ttcctcggtt	accagattga	1860
tgaaaatttc	atgaagattg	aagaaagcag	atggaaagaa	ttaaggactg	taatcaagaa	1920
aataaaagta	ggagaatggg	atgactggaa	atgtattcaa	agatttgtgg	ggcatttgaa	1980
ttttgttttg	ccttttacta	aaggtaatat	tgaaatgtta	aaaccaatgt	atgctgctat	2040

tactaaccaa gtaaacttta gcttctcttc atcctatagg actttgttat ataaactaac	2100
aatgggtgtg tgtaaattaa gaataaagcc aaagtcctct gtacctttgc cacgtgtagc	2160
tacagatgct accccaacac atggcgcaat atcccatatc accggcggga gcgcagtgtt	2220
tgctttttca aaggtcagag atatacatgt tcaggaacta ttgatgtctt gtttagccaa	2280
gataatgatt aaaccacgtt gtctcttatc tgattcaact tttgtttgcc ataagcgtta	2340
tcagacgtta ccatggcatt ttgctatgtt ggccaaacaa ttgctcaaac cgatacaatt	2400
gtactttgtc ccgagcaa ataatcctgc tgacggccca tccaggcaca aacctcctga	2460
ttggacggct tttccataca cccctctctc gaaagcaata tatattccac ataggctatg	2520
tggaacttaa gaattacacc cctctccttc ggagctgctt gccaagggtat ctttacgtct	2580
acattgctgt tgtcgtgtgt gactgtacct ttggtatgta ccattgttta tgattcttgc	2640
ttatatatgg atatcaatgc ttctagagcc ttagccaatg tgtatgatct accagatgat	2700
ttctttccaa aaatagatga tcttgttaga gatgctaaag acgctttaga gccttattgg	2760
aaatcagatt caataaagaa acatgttttg attgcaactc actttgtgga tctcattgaa	2820
gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata	2880
cctcccacta ctactcctgt tccaccgggt tatcttattc agcacgagga agctgaagag	2940
atacctttgg gagatttatt taaacaccaa gaagaaagga tagtaagttt ccaacccgac	3000
tatccgatta cggctagaat t	3021

<210> 6  
 <211> 984  
 <212> DNA  
 <213> duck

<220>  
 <221> CDS  
 <222> (1)..(984)

<400> 6 atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly 1 5 10 15	48
gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly 20 25 30	96
act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp 35 40 45	144
cat gtg caa aca atg gag gag ata aac acc ctc cag aat cag gga gct His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala 50 55 60	192
tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct 3	240

Trp 65	Pro	Ala	Gly	Ala	Gly 70	Arg	Arg	Val	Gly	Leu 75	Ser	Asn	Pro	Thr	Pro 80	
caa Gln	gag Glu	att Ile	cct Pro	cag Gln 85	ccc Pro	cag Gln	tgg Trp	act Thr	ccc Pro 90	gag Glu	gaa Glu	gac Asp	caa Gln	aaa Lys 95	gca Ala	288
cgc Arg	gaa Glu	gct Ala	ttt Phe 100	cgc Arg	cgt Arg	tat Tyr	caa Gln	gaa Glu 105	gaa Glu	aga Arg	cca Pro	ccg Pro	gaa Glu 110	acc Thr	acc Thr	336
acc Thr	att Ile	cct Pro 115	ccg Pro	tct Ser	tcc Ser	cct Pro	cct Pro 120	cag Gln	tgg Trp	aag Lys	cta Leu	caa Gln 125	ccc Pro	ggg Gly	gac Asp	384
gat Asp	cca Pro 130	ctc Leu	ctg Leu	gga Gly	aat Asn	cag Gln 135	tct Ser	ctc Leu	ctc Leu	gag Glu	act Thr 140	cat His	ccg Pro	cta Leu	tac Tyr	432
cag Gln 145	tca Ser	gaa Glu	cca Pro	gcg Ala	gtg Val 150	cca Pro	gtg Val	ata Ile	aaa Lys	act Thr 155	ccc Pro	ccc Pro	ttg Leu	aag Lys	aag Lys 160	480
aaa Lys	atg Met	tct Ser	ggg Gly	acc Thr 165	ttc Phe	ggg Gly	gga Gly	ata Ile	cta Leu 170	gct Ala	ggc Gly	cta Leu	atc Ile	gga Gly 175	tta Leu	528
ctg Leu	gta Val	agc Ser	ttt Phe 180	ttc Phe	ttg Leu	ttg Leu	ata Ile	aaa Lys 185	att Ile	cta Leu	gaa Glu	ata Ile	ctg Leu 190	agg Arg	agg Arg	576
cta Leu	gat Asp	tgg Trp 195	tgg Trp	tgg Trp	att Ile	tct Ser	ctc Leu 200	agt Ser	tct Ser	cca Pro	aag Lys	gga Gly 205	aaa Lys	atg Met	caa Gln	624
tgc Cys	gct Ala 210	ttc Phe	caa Gln	gat Asp	act Thr	gga Gly 215	gcc Ala	caa Gln	atc Ile	tct Ser	cca Pro 220	cat His	tac Tyr	gta Val	gga Gly	672
tct Ser 225	tgc Cys	ccg Pro	tgg Trp	gga Gly	tgc Cys 230	cca Pro	gga Gly	ttt Phe	ctt Leu	tgg Trp 235	acc Thr	tat Tyr	ctc Leu	agg Arg	ctt Leu 240	720
ttt Phe	atc Ile	atc Ile	ttc Phe	ctc Leu 245	tta Leu	atc Ile	ctg Leu	cta Leu	gta Val 250	gca Ala	gca Ala	ggc Gly	ttg Leu	ctg Leu 255	tat Tyr	768
ctg Leu	acg Thr	gac Asp	aac Asn 260	ggg Gly	tct Ser	act Thr	att Ile	tta Leu 265	gga Gly	aag Lys	ctc Leu	caa Gln	tgg Trp 270	gcg Ala	tcg Ser	816
gtc Val	tca Ser	gcc Ala 275	ctt Leu	ttc Phe	tcc Ser	tcc Ser	atc Ile 280	tct Ser	tca Ser	cta Leu	ctg Leu	ccc Pro 285	tcg Ser	gat Asp	ccg Pro	864
aaa Lys	tct Ser 290	ctc Leu	gtc Val	gct Ala	tta Leu	acg Thr 295	ttt Phe	gga Gly	ctt Leu	tca Ser	ctt Leu 300	ata Ile	tgg Trp	atg Met	act Thr	912
tcc Ser 305	tcc Ser	tct Ser	gcc Ala	acc Thr	caa Gln 310	acg Thr	ctc Leu	gtc Val	acc Thr	tta Leu 315	acg Thr	caa Gln	tta Leu	gcc Ala	acg Thr 320	960
ctg	tct	gct	ctt	ttt	tac	aag	agt									984

Leu Ser Ala Leu Phe Tyr Lys Ser  
325

<210> 7  
<211> 328  
<212> PRT  
<213> duck

<400> 7

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly  
1 5 10 15

Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly  
20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp  
35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala  
50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro  
65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala  
85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr  
100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp  
115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
145 150 155 160

Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu  
165 170 175

Leu Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg  
180 185 190

Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln  
195 200 205

Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly  
5

210

215

220

Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu  
225 230 235 240

Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr  
245 250 255

Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser  
260 265 270

Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro  
275 280 285

Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr  
290 295 300

Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr  
305 310 315 320

Leu Ser Ala Leu Phe Tyr Lys Ser  
325

<210> 8  
<211> 501  
<212> DNA  
<213> duck

<220>  
<221> CDS  
<222> (1)..(501)

<400> 8  
atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg 48  
Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu  
1 5 10 15

gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta 96  
Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu  
20 25 30

gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc 144  
Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys  
35 40 45

gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct 192  
Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser  
50 55 60

tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt 240  
Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe  
65 70 75 80

atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg 288  
Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu  
6

85								90				95				
acg	gac	aac	ggg	tct	act	att	tta	gga	aag	ctc	caa	tgg	gcg	tcg	gtc	336
Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val	
			100					105					110			
tca	gcc	ctt	ttc	tcc	tcc	atc	tct	tca	cta	ctg	ccc	tcg	gat	ccg	aaa	384
Ser	Ala	Leu	Phe	Ser	Ser	Ile	Ser	Ser	Leu	Leu	Pro	Ser	Asp	Pro	Lys	
		115					120					125				
tct	ctc	gtc	gct	tta	acg	ttt	gga	ctt	tca	ctt	ata	tgg	atg	act	tcc	432
Ser	Leu	Val	Ala	Leu	Thr	Phe	Gly	Leu	Ser	Leu	Ile	Trp	Met	Thr	Ser	
	130					135					140					
tcc	tct	gcc	acc	caa	acg	ctc	gtc	acc	tta	acg	caa	tta	gcc	acg	ctg	480
Ser	Ser	Ala	Thr	Gln	Thr	Leu	Val	Thr	Leu	Thr	Gln	Leu	Ala	Thr	Leu	
145					150					155					160	
tct	gct	ctt	ttt	tac	aag	agt										501
Ser	Ala	Leu	Phe	Tyr	Lys	Ser										
				165												

<210> 9  
 <211> 167  
 <212> PRT  
 <213> duck

<400> 9

Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu	Leu	
1				5					10					15		
Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg	Leu	
			20					25					30			
Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln	Cys	
		35					40					45				
Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly	Ser	
	50					55					60					
Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu	Phe	
65					70					75					80	
Ile	Ile	Phe	Leu	Leu	Ile	Leu	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr	Leu	
			85						90					95		
Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val	
			100					105					110			
Ser	Ala	Leu	Phe	Ser	Ser	Ile	Ser	Ser	Leu	Leu	Pro	Ser	Asp	Pro	Lys	
		115					120					125				
Ser	Leu	Val	Ala	Leu	Thr	Phe	Gly	Leu	Ser	Leu	Ile	Trp	Met	Thr	Ser	
	130					135					140					

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu  
 145 150 155 160

Ser Ala Leu Phe Tyr Lys Ser  
 165

<210> 10  
 <211> 483  
 <212> DNA  
 <213> duck

<220>  
 <221> CDS  
 <222> (1)..(483)

<400> 10  
 atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga 48  
 Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly  
 1 5 10 15  
 gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg 96  
 Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly  
 20 25 30  
 act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac 144  
 Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp  
 35 40 45  
 cat gtg caa aca atg gag gag ata aac acc ctc cag aat cag gga gct 192  
 His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala  
 50 55 60  
 tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct 240  
 Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro  
 65 70 75 80  
 caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca 288  
 Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala  
 85 90 95  
 cgc gaa gct ttt cgc cgt tat caa gaa gaa aga cca ccg gaa acc acc 336  
 Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr  
 100 105 110  
 acc att cct ccg tct tcc cct cct cag tgg aag cta caa ccc ggg gac 384  
 Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp  
 115 120 125  
 gat cca ctc ctg gga aat cag tct ctc ctc gag act cat ccg cta tac 432  
 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
 130 135 140  
 cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag 480  
 Gln Ser Glu Pro Ala Val Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
 145 150 155 160  
 aaa 483  
 Lys



<210> 11  
 <211> 161  
 <212> PRT  
 <213> duck

<400> 11

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly  
 1 5 10 15

Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly  
 20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp  
 35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala  
 50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro  
 65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala  
 85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr  
 100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp  
 115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
 130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
 145 150 155 160

Lys

<210> 12  
 <211> 501  
 <212> DNA  
 <213> duck

<220>  
 <221> CDS  
 <222> (1)..(501)

<400> 12

atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu 1 5 10 15	48
gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu 20 25 30	96
gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys 35 40 45	144
gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser 50 55 60	192
tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe 65 70 75 80	240
atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu 85 90 95	288
acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val 100 105 110	336
tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys 115 120 125	384
tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser 130 135 140	432
tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg ctg Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu 145 150 155 160	480
tct gct ctt ttt tac aag agt Ser Ala Leu Phe Tyr Lys Ser 165	501

<210> 13  
 <211> 167  
 <212> PRT  
 <213> duck

<400> 13

Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu 1 5 10 15
Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu 20 25 30
Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys 35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser  
 50 55 60  
 Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe  
 65 70 75 80  
 Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu  
 85 90 95  
 Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val  
 100 105 110  
 Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys  
 115 120 125  
 Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser  
 130 135 140  
 Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu  
 145 150 155 160  
 Ser Ala Leu Phe Tyr Lys Ser  
 165